

**These are the steps required to use CIPRES REST from Geneious. If you have questions or problems, please contact me at [mmiller@ucsd.edu](mailto:mmiller@ucsd.edu))**

**Step 1. Create an account at CIPRES REST. (one time only)**

Visit: <https://www.phylo.org/restusers/register.action> to register.

**Step 2. Install the MrBayes\_CIPRES plugin. (one time only)**

Go to [http://www.phylo.org/geneious\\_mrbayes](http://www.phylo.org/geneious_mrbayes)

Download the application MrBayes\_CIPRES.gplugin and the file geneious\_client.conf

Move the file geneious\_client.conf to your home directory.

*In Windows, this is C:/users/your\_user\_name*

*In MacOS; use the Go pull-down menu from the menu bar to go to the Home folder, open the Finder application and press cmd-shift-H, or open a terminal window and type "cd" to find your home directory.*

Edit the file geneious\_client.conf so your username and password are entered correctly.

Start Geneious and drag the MrBayes\_CIPRES add-in onto the Geneious work area.

Geneious will prompt you as to whether or not you want to use this add-in. Accept the add-in.

**Step 3. Run a MrBayes Job on CIPRES:**

Once the add-in is loaded, select Tools/MrBayes\_CIPRES from the top menu.

Specify the folder for your MrBayes results.

If you see the message "Please check 'geneious\_cipres.conf' file in your home directory", then the connection to CIPRES REST API was not established correctly. Likely causes are your password or login name don't match, or the geneious\_cipres.conf file is not in your home directory. *It is important to resolve this before proceeding. Otherwise Geneious will crash when you try to run a job.*

Select your desired sequence alignment from your data.

In the top menu, select Tree

Once the Tree option opens up, select MrBayes\_CIPRES as the tree tool.

Configure the run using the form provided, and if needed, use the "Custom MrBayes block" option to add additional parameters.

Click OK to submit.

You will see a message saying the job is being submitted.

The message will be "Performing MrBayes\_CIPRES"

When your job is completed, you will receive an email.

**Step 4. Download your CIPRES REST results to your local machine (each time).**

To import your results into Geneious, go to Tools/MrBayes\_CIPRES

Your jobs will be displayed.

You can monitor progress with the Update\_list button.

Highlight the completed job.

Click download, and specify the folder where you would like your job results to end up.

**Step 5. Import your results into Geneious (each time)**

Once the download is complete, locate the job results on your machine. Now you must put those results into Geneious. To do this, drag the folder that contains your job results from its location on your machine to a folder in the Geneious interface.

When you do this, Geneious will warn there are files that cannot be processed or recognized, because not all CIPRES files are known to Geneious. Just click through the warning messages. All the files you need to analyze your job results will appear in the Geneious folder you specified, and ready for further analysis.